

SEQUENCE LISTING

<110> Novartis AG
Novartis Research Foundation

<120> Gene involved in epigenetic gene silencing

<130> S-31005A

<140>
<141>

<150> GB 9914623.5
<151> 1999-06-23

<160> 33

<170> PatentIn Ver. 2.1

<210> 1
<211> 10329
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> intron
<222> (1009)..(1295)

<220>
<221> intron
<222> (2551)..(2673)

<220>
<221> intron
<222> (2753)..(2867)

<220>
<221> intron
<222> (3114)..(3506)

<220>
<221> intron
<222> (3681)..(3973)

<220>
<221> intron
<222> (4896)..(4975)

<220>
<221> intron
<222> (5218)..(5777)

<220>
<221> intron
<222> (5883)..(6082)

<220>
<221> intron
<222> (7481)..(7615)

<220>
<221> intron
<222> (7772)..(7914)

<220>
 <221> intron
 <222> (8071)..(8153)

<220>
 <221> intron
 <222> (8319)..(8451)

<220>
 <221> intron
 <222> (8630)..(8718)

<220>
 <221> intron
 <222> (8919)..(9000)

<220>
 <221> intron
 <222> (9212)..(9284)

<400> 1
 aatattttaag tttggtttat attctttcta gtaatctttg aaatattgta agagataatg 60
 cttctaataa ataacattgg atttattgga attaatgtat tgaaaaaact atgcaaatac 120
 tacagtgtat tttggaacga ccaaaatgat atatgtaaac tttcgttcta gtcttctaca 180
 tagtgtaata ggatagcggg caaggttgat cgactctaaa cattatgggt acgtaattcc 240
 gcagtgggta cagtctactg tcgaggccaa actggtaatt aaacgtttga agtttagaga 300
 aatattttga tgatgagtac cacaatcaaa gatgataggt gttaatcact gtaaaaatgt 360
 tgattgaata ctacgaatgc agaacatata catattttta atctctttgg aatttttggt 420
 tttgttttta tcatttttga atacacgaag agctcagtta ttttcatat tgtatatgaa 480
 tttgttctat ttaatcttca attctagcaa catactctta tgctaattcg tttcatattt 540
 tagtatagta taaaaattac aaatttcaaa acaaaactata agtaatatac taacatagtc 600
 ggtgtaacat ttcgttaatt tcacataaca tatgttaatt acatatgtac actatttttg 660
 aagtatttta taacttaaaa tatataaatt taaatctaag aaatcacaag catgagtttt 720
 tccttccggg aatcgtaaaa tcaaaaatcg ctgcctcgag aaacgccggg gctagaagag 780
 gaaagtaccg tacataatcc tgcaaaccca attctcgtct tcttcaaact cagttttccg 840
 aaaccccaaa caccgcgagg attgcatggc ctgaagaacc acttaatcga gaattgtgct 900
 ggaatttcta aattttccct cgcggttttc tttcacactc tcggaatcgg aaatttccac 960
 caagctccgt caagcgatag attctgacaa ttacacactt tcgcgcagggt atgcttcctt 1020
 ccctgtttta ggttggtgtt aatctatcgg tgaatcgaag gttttgggccc tcgggctttg 1080
 cgtttttaggt ttttcagaga atcttatcta ctgggggatg gatcttaggc gtttgtaga 1140
 tgtaactcat tagttttgca tataggaatt ttgatttgaa agtttaggtcg ccggatttgt 1200
 agacattttg tttgatggtc ttcttcgggtg ctacatttct ttgtttttaa gtgcttgatt 1260
 tgggtgctaa ggtcctttcc gttgcgtgct ctcaagtgaat atgaagaaag atgaaaagat 1320
 tgggttgacg gggagaacca ttacaccag atccctagca gcttcaattc ctgcctcagt 1380
 tgaacaagaa acccctggtt tgaggaggtc aagccggggg acaccatcta cgaaggtaat 1440
 aactccagct tctgctacta gaaagtcaga gagactggct ccctcacctg cttcagtttc 1500
 aaaaaagtc ggtggaatcg tcaagaattc cacaccaagt tctttgcgaa ggtccaatag 1560
 ggggaagact gaagtatcct tgcagagttc caaaggatca gataattcta tcaggaaagg 1620
 agatacttca ccggatattg agcagagaaa ggatagtgtt gaagagtcga cagataagat 1680
 caagcctata atgtcagccc gaagtacag ggcattgttt agagggaagc tcaagggaatc 1740
 tgaggcatta gttgatgctt ccccaaatga agaggaaacta gtagttgttg gttgttctcg 1800
 ccgcatacct gcaggcaatg atgatgttca aggtaaaaca gattgtccac cactgcaga 1860
 tgcaggatca aaaaggctgc cagttgacga aactagtttg gacaagggca ctgattttcc 1920
 tttgaaatca gttacggaga ccgagaagat agtgcttgat gcatcccca tagttgaaac 1980
 tggggatgac agtggttatag gttcaccatc tgagaattta gagacacaaa agcttcaaga 2040
 tggtaagaca gattgttcac cactgcaaa tgcagaatcg aaaacgctgc cagttgggtga 2100
 aactagttta gaaaagaat atccacaaaa gtttcaagat gataacacag attgtctacc 2160
 acctgcaaat gcagaatcaa aaaggctgcc agttggcgaa actagtttag aaaaggacac 2220
 tgattttcct ttgaaatcaa ctacggagac tggaaagatg gttctttatg catcccccat 2280
 agttgaaact agggatgaca gcgttatatg ttaccatctt acaaatttag aaacccaaaa 2340
 gcttcttgct agtaaaactg gcttagaaac cgacatagtt ttgcctttga aaagaaaaag 2400
 agacactgca gaaattgagc tggatgcatg tgctacagtt gcaaatggag atgatcacgt 2460
 tatgagttct gatggggatc ttccatctcc atctgggtgc aaaaatgata atcgacctga 2520

aatgtgcaac	acgtgtaaaa	aacggcaaaa	gtaagagttt	ttttagtggt	gtctgtctat	2580
tgaaacgac	tgccaatggt	gaatgttggg	cagatgggtt	tgattcttag	gatatatggt	2640
ctgtattgta	atgagttggt	caaaattttg	aaggggtcaac	ggtgattgtc	aaaataggag	2700
tgtttgtctc	tgcaattgtc	agccagttgt	agaactctgat	aacgtgacac	aggttggttt	2760
ctaattactt	tcggagaccc	gttaatcagt	ggactcttaa	atagttagat	actagattta	2820
cttatccttt	tacttgtaat	ctgcaattct	attttgcatt	tgattaggat	atgaaagaaa	2880
ctggaccagt	tacgagcaga	gaatatgagg	agaacgggca	aatacaacat	ggtaaatcaa	2940
gtgatcccaa	attctattct	tcggtgtacc	cagagtattg	ggttcctgtg	cagctatcag	3000
atgtacagct	ggagcaatac	gtcagactc	tcttctccaa	atccttatct	ctttcttcac	3060
tttcgaagat	tgatcttgga	gctctagaag	aaactctcaa	ttctgtaaga	aaagtaagtt	3120
acttgatttt	aaaaacactt	attcttcaat	gcacttggtga	gttaagtacc	cagttattac	3180
tgggtgataag	ataaagaaa	caatagaaaa	attgataagg	tgttcaccgc	attgcagcca	3240
aaaaaacaat	tctgtgttcc	atgctttcaa	gaggttggtca	catagggtgt	atgcctttct	3300
gtttgatggt	tggtagagca	aaggttttgg	gtctatttgt	tttatgcttt	tttgaaacac	3360
atagaacctg	gcaaaactga	cagttttggg	gttgcttaga	tatacgacta	ttgtcgggtca	3420
gcattcacatt	ttctcaaggc	ctcttctcgc	atgttaaatgt	gtgaatatat	taaaatcttc	3480
tttatgtggt	tgcaacttgt	tgacagacct	gtgacctacc	atacgttatg	gatgcattct	3540
tgaacaact	gctcaccaag	aatctggagt	tgcatgaaat	cctggatgta	gaaattaaag	3600
cgagcgggaa	acttcacctc	cttgataaaa	tgcttactca	tataaaaaag	aatgggttaa	3660
aagcagttgt	cttctaccag	gtgcattttc	tattacttgc	gaatgtgaat	agctctatgt	3720
ttgtcatgaa	tacgtcacct	tgtgcattct	caatatatgt	gcatttttct	tttgacaatg	3780
gaattctgtc	ttgtattgaa	atttgagtgg	gatgaaagta	tgctttttat	cggtcaatta	3840
tgaagtgtaa	gttagccttc	agcagtcagc	tagcattatg	agatatgctg	aactaaaatg	3900
tttcttttct	cttcttttct	tttcgttata	tgtgcctcat	gtatgtttga	attacagttt	3960
ttattttcag	caggcaacac	aaacccctga	agggcttctg	cttggttaata	ttctcgaaga	4020
ttttgtgggt	caaaagattt	gtccaaaatc	ttatgagcat	gggatataat	cctcaaagaa	4080
gaactccgct	ataaacaatt	tcaacaagga	gagtcaatgc	tgtgttctgc	tggtggaaac	4140
acgtgcctgc	agtcaaacca	ttaaactctt	gcgagctgat	gcgtttattc	tttttggaa	4200
cagcttgaat	ccatcgcatg	atgttaagca	cgtagagaag	ataaaaaatc	agtcattgtc	4260
tgaagaact	aagatattcc	gattgtactc	agtatgtaca	gttgaagaaa	aagccctgat	4320
tctggctagg	caaaaatagc	ggcaaaaata	agctgtagag	aacctaaacc	gctctctcac	4380
gcacgcactg	ctcatgtggg	gggcgtcata	cttatttgat	aaactggatc	attttcacag	4440
cagtgaact	ccagattcag	gagtttcatt	tgaacaatct	attatggacg	gcgtgattca	4500
tgaattctcg	tccatacttt	cttccaaagg	tggaagaa	aatgaagtca	agctgtgtct	4560
acttttggag	gccaagcatg	ctcagggaa	ttacagcagt	gattctactc	tatttgggtga	4620
agaccatatt	aagttgtcag	atgaagagag	tccaaatata	ttttggtcaa	agctgttggg	4680
gggaaaaaat	cctatgtgga	aatacccttc	agatactccc	caaaggaatc	gaaaacgagt	4740
tcagtatatt	gagggttctg	aagcaggtcc	caaaaactgg	gatgggtggaa	atgcaaagaa	4800
gcgaagaag	gcttctgatg	atgtcactga	tccccgggtc	actgatccgc	cagtagatga	4860
tgatgaaaga	aaggcctctg	ggaaggatca	catgggtaaa	atagtttaat	ttctgctccg	4920
atacctctag	tgttcattga	ttatgcaact	actttgctga	ctatctttcc	tacaggggct	4980
ttggagtcac	caaaagtcac	aacactccag	tcattcatgta	aatcttctgg	tacagatggt	5040
acattggatg	gaaatgatgc	ttttggcttg	tattctatgg	gcagccatat	ctctggaatc	5100
ccagaggata	tgtagctag	tcaagattgg	gggaaaatac	cggatgaatc	acagaggagg	5160
ctccacactg	ttttaagcc	gaagatggca	aaactttgcc	aagttttgca	tctttcagta	5220
agtggccttt	ttcacctcca	caacttattt	tagccttgca	tatgcttata	tatagctgat	5280
tgaactgtta	gttggtacct	gatttctgt	tacagccaaa	tgtgagagtt	ttattcttca	5340
actatatcca	tccgtttaag	catattttat	ttcttatatc	tggcttcggt	accaatgcac	5400
tgtaaaaatg	agcaactgct	gcacaaaaca	gtaggtagtt	atgtgcctca	tgctattcat	5460
tgtttattga	agcaaagaaa	tttctgtcta	ctttacatga	tccatctgtg	ggagtatata	5520
actatatata	accttaggcc	tttgtacctg	gctgatcaaa	gacatgtcaa	aagtttatct	5580
gttcgctggt	ggtatagaaa	ctaatacagt	gtctgatgct	attttaaggt	agtcctatgt	5640
cttcacatat	tggctaatag	atgtttccgc	tgtcgtgtcc	atatacttct	gtgattatca	5700
cggtgctccg	tctatcaaaa	ttgtactaaa	aggtattttg	caatgtgtga	ttggttaaca	5760
gattattttg	ttttcaggat	gcttgacaaa	gcattggtcgg	aaattttctc	gaatatgtta	5820
ttgaaaatca	ccgaatctac	gaagagccag	ccactacttt	tcaggcattc	cagatagccc	5880
tggtatgaca	gcatttactt	tgataattta	tgcatgtttt	ccttcatcat	ctgcctttgt	5940
ttagaatgtc	ctcagaaggc	agcactcctt	tagttttaac	tttccaatca	taggattcaa	6000
atatccatta	actggccttt	gatcgcgtca	taatatatga	atagttgaca	tactgaatac	6060
gttgtaataa	atgcattttc	agagtgtgat	tgacgccttg	ttggtaaagc	aaattcttag	6120
ccacaaagaa	tctctgggtc	gtgcaaatc	tgaattagct	ttcaaatgct	ctagagtaga	6180
ggtggattat	atttattcga	tattgtcctg	catgaagagt	ctgttcctgg	agcatacaca	6240
aggtttgcag	ttcgattgct	ttggtactaa	ttctaaacag	tcagtgggtta	gcacaaaact	6300
agtaaatgaa	agtctctcag	gggtcacagt	gcgtgacgaa	aagattaata	cgaagtcgat	6360

gcgaaatagc	tcagaggatg	aagagtgc	gactgagaag	agatgtagcc	attatagcac	6420
agcaacaaga	gatatcgaaa	agactattag	tggcataaaa	aagaaataca	agaagcaagt	6480
gcaaaagc	gtacaagagc	atgaggaaaa	gaaaatggag	ctgttaaata	tgtatgcaga	6540
caagaagcag	aaacttgaaa	ctagtataag	tgtggaagca	gcagtaattc	gtattacctg	6600
ttcacggacc	agtactcaag	tgggtgatct	caaaactgctg	gatcataatt	atgaaagaaa	6660
gtttgatgaa	atcaaaagt	agaaaaatga	atgcctcaaa	agtctggagc	aaatgcacga	6720
ggttgcaag	aagaagtgg	ctgaggatga	agcctgttgg	attaatcgga	taaagagctg	6780
ggcagctaaa	ttaaaagttt	gtgttcccat	tcaaagtggc	aataacaagc	atttttagtg	6840
ttcatcaaac	atttcccaaa	atgctcctga	tgtacaaatt	tgcaataatg	ctaacggtga	6900
agctacttac	gctgatacga	attgcatggc	ttccaagggt	aatcaagtgc	cagaagcaga	6960
aaacacatta	ggaaccatgt	cgggtggcag	cactcaacaa	gttcatgaaa	tgggtggatgt	7020
aagaaatgac	gagacaatgg	atgtctcagc	tttgtctcgt	gaacagctta	caaagagcca	7080
gtccaatgag	cacgcttcta	tcactgtgcc	tgagattttg	attcctgctg	actgtcaaga	7140
ggaatttgcg	gccttgaacg	tgcatttgtc	agaagaccag	aattgtgaca	gaataacatc	7200
tgcggcatca	gatgaagatg	tttcatcaag	ggtgccagag	gtatcccagt	cactcgaaaa	7260
cttttctgcc	tcccccgagt	tttctctaaa	tagagaggag	gctttggtta	caacagaaaa	7320
tagaagaaca	agtcattgtg	gttttgatac	tgataacatt	ttggaccagc	agaatagaga	7380
agattgttct	cttgaccaag	agattcctga	cgagttagcg	atgcctgtgc	aacatcttgc	7440
gtctgtggtg	gagactaggg	gtgctgctga	atctgatcag	gtacttactg	gccctgtaga	7500
atagttgatg	ccttgttcat	ttaatctttt	ctaattgttca	ttcttgcttt	cttgaaaaata	7560
acgggtagtg	atcagatgtc	tttttttctc	ttattaaatt	cacttttctg	gacagtatgg	7620
tcaagatata	tgtcctatgc	cttcttcact	ggctggaaaag	caacctgacc	cagcagcaaa	7680
cactgagagc	gaaaatcttg	aagaagcaat	tgagcctcag	tctgctggtt	cagaaacagt	7740
agagactact	gattttgctg	catcacatca	ggtccctatt	gaagactttc	cttttttact	7800
agtttaaagt	tatcaatctg	tgttatgttc	attctaagtt	tccgtgagaa	aaagggtggg	7860
aaatgtggtt	actgatcaag	tctcgttgtt	gttttaaatt	gactcttttg	acagggtgat	7920
caagttacat	gtcctttgct	atcttcaccg	actggaaatc	agcctgcgcc	agaagcaaat	7980
attgaaggcc	aaaatatcaa	cacatcagct	gagcccatg	tagcgggtcc	agatgcagta	8040
gagagtgggtg	attatgcagt	aatagatcag	gttattgcct	taactaaaga	caaagtgtct	8100
ttgttgttta	aaagtcttac	atctttgtaa	tgctcgttct	ggatatcctg	caggaaacaa	8160
tgggtgtctca	ggaatgcagc	tctctgccat	ctggatcggt	tggaaactcag	tctgacctag	8220
gagcaaacat	tgagggtcag	aatgtcacia	cagtggctca	acttcccaca	gatggatcag	8280
atgcagttgt	aaccgggtga	tctcctgtat	cagatcaggt	acctgcctct	gctcaaggac	8340
tttcttatgt	gttggtttta	aggtctagtc	cttagtaatg	ttgaaactaa	gcaaacagtg	8400
gatagtgatc	atatggttat	ttttgcttgt	gaatttaata	tttctggaca	gtgtgccccag	8460
gatgcattct	ctatgccatt	atcttcgcct	ggaaatcacc	ctgatacagc	agttaatatc	8520
gagggtttag	ataacacatc	agtagctgag	cctcatataa	gtggatcaga	tgcatgtgaa	8580
atggaaattt	cagaacctgg	tccccaagta	gagcgggtcaa	cctttgcaag	tcagtaactg	8640
ccttgggcat	ttttaagtat	cacctaggtc	gacatatgtg	attgccaaac	agctaacaag	8700
gagatgcctt	ttgtgcagat	cttttccatg	aagggtggcgt	ggagcattca	gcagggtgtaa	8760
cagctcttgt	tccatcactt	cttaacaatg	gtacggaaca	gattgccgtt	caacctgttc	8820
ctcaaatacc	ttcccctgtg	ttcaacgacc	cgtttctgca	tgaactggag	aagttgcgga	8880
gagaatcaga	gaactctaaag	aagacttttg	aagaaaaagt	cagtttccct	cattaccag	8940
ttacctcttg	ttttggttta	ttttctagct	gcccattgac	tctcagttgc	ttgtgagcag	9000
aaatcaatct	tgaaagctga	actcgagagg	aagatggctg	aagtacaagc	agagtttcga	9060
agaaaatttc	atgaggtaga	agccgagcat	aacaccagaa	cgacaaagat	agagaaggat	9120
aagaatcttg	ttataatgaa	caaaactgtg	gcgaatgcgt	tcttgtccaa	atgtactgac	9180
aagaaggat	ctcccctcagg	agctccaagg	ggtaagtgtc	gaataatata	gcaaattgggt	9240
tttaaaaata	aggcgacgaa	gtcataatag	cactttttct	ccaggtaaaa	ttcagcagct	9300
agcacagaga	gcagcacaa	tgagtgcact	gagaaattac	attgtctctc	agcagcttca	9360
ggcatcttct	tttctgtctc	ctgctctggt	ttcggctcct	ctgcaacttc	agcaatcatc	9420
atttctgtct	cctggtccgg	ctcctctgca	gccctaggca	tcttcgtttc	cttcttcagt	9480
ctctcgctca	tcagcccttc	ttctgaattt	tgcggtctgt	ccaatgcctc	agcccagaca	9540
gcctctcata	tccaacatag	ctccaactcc	atcagttact	cctgcaacaa	atccagggtct	9600
gcgttctctc	gcaccacacc	taaactcata	tagaccatcc	tcttcaactc	ccgtcgccac	9660
agctactcca	acctcgtcag	tgccctctca	agctttgaca	tattcagctg	tgtcaattca	9720
gcagcagcaa	gaacaacaac	cgcaacagag	cttgagcagt	ggattgcaga	gcaacaatga	9780
agtggtttgt	ctttctgacg	acgagtgacc	taagaggaga	gatggttagg	gtcttagtta	9840
ttgattttta	cagagttaat	aatagtatat	atatatatgt	ataagtaggt	tacctaatct	9900
ctgtcgttaa	tctaatttag	tgagttagga	accgactcgt	tggctaagggt	ctctcctttt	9960
gaaacgcaac	gttctacttt	catgtatata	aatacagctc	gatcacacaa	cacaaattga	10020
tgattgaaaa	tactactgat	tttaactttat	agaaaaacca	aattatagag	cgacaacttt	10080
ataaacatgt	caaacttcga	agttaaaatt	taagacccca	taattttaca	attatagatt	10140
ttaatactcc	aactattttg	tgatgttaaa	agaagtatcc	gagtcctttc	tttccagttt	10200

ccccaccgtc ccatgactcc cccagccagt agaaaaagcc aaaaaagtaa acaaaaagtc 10260
 gttaaaaaag tttaaattaaa aaaaaaatag atagttgacg tttactaaag tgatttgaat 10320
 tgaacaatt 10329

<210> 2
 <211> 6571
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (310)..(6312)

<400> 2
 cacaagcatg agtttttcct tccggtaatc gtaaaatcaa aaatcgctcg ctcgagaaac 60
 gccggtgcta gaagaggaaa gtaccgtaca taatcctgcg aaccaattc tcgtcttctt 120
 caaactcagt tttccgaaac cccaaacacc gcgaggattg catggcctga agaaccactt 180
 aatcgagaat tgtgctggaa ttctcaaatt ttccctcgcg tttttctttc acactctcgg 240
 aatcggaat ttccaccaag ctccgtcaag cgatagattc tgacaattac acactttcgc 300
 gcagtgaat atg aag aaa gat gaa aag att ggt ttg acg ggg aga acc att 351
 1 5 10
 Met Lys Lys Asp Glu Lys Ile Gly Leu Thr Gly Arg Thr Ile

tac acc aga tcc cta gca gct tca att cct gcc tca gtt gaa caa gaa 399
 Tyr Thr Arg Ser Leu Ala Ala Ser Ile Pro Ala Ser Val Glu Gln Glu
 15 20 25 30

acc cct ggt ttg agg agg tca agc cgg ggg aca cca tct acg aag gta 447
 Thr Pro Gly Leu Arg Arg Ser Ser Arg Gly Thr Pro Ser Thr Lys Val
 35 40 45

ata act cca gct tct gct act aga aag tca gag aga ctg gct ccc tca 495
 Ile Thr Pro Ala Ser Ala Thr Arg Lys Ser Glu Arg Leu Ala Pro Ser
 50 55 60

cct gct tca gtt tca aaa aag tcc ggt gga atc gtc aag aat tcc aca 543
 Pro Ala Ser Val Ser Lys Lys Ser Gly Gly Ile Val Lys Asn Ser Thr
 65 70 75

cca agt tct ttg cga agg tcc aat agg ggg aag act gaa gta tcc ttg 591
 Pro Ser Ser Leu Arg Arg Ser Asn Arg Gly Lys Thr Glu Val Ser Leu
 80 85 90

cag agt tcc aaa gga tca gat aat tct atc agg aaa gga gat act tca 639
 Gln Ser Ser Lys Gly Ser Asp Asn Ser Ile Arg Lys Gly Asp Thr Ser
 95 100 105 110

ccg gat att gag cag aga aag gat agt gtt gaa gag tcg aca gat aag 687
 Pro Asp Ile Glu Gln Arg Lys Asp Ser Val Glu Glu Ser Thr Asp Lys
 115 120 125

atc aag cct ata atg tca gcc cga agt tac agg gca ttg ttt aga ggg 735
 Ile Lys Pro Ile Met Ser Ala Arg Ser Tyr Arg Ala Leu Phe Arg Gly
 130 135 140

aag ctc aag gaa tct gag gca tta gtt gat gct tcc cca aat gaa gag 783
 Lys Leu Lys Glu Ser Glu Ala Leu Val Asp Ala Ser Pro Asn Glu Glu
 145 150 155

gaa Glu	cta Leu	gta Val	gtt Val	gtt Val	ggt Gly	tgt Cys	tct Ser	cgc Arg	cgc Arg	ata Ile	cct Pro	gca Ala	ggc Gly	aat Asn	gat Asp	831
160						165					170					
gat Asp	gtt Val	caa Gln	ggt Gly	aaa Lys	aca Thr	gat Asp	tgt Cys	cca Pro	cca Pro	cct Pro	gca Ala	gat Asp	gca Ala	gga Gly	tca Ser	879
175					180					185					190	
aaa Lys	agg Arg	ctg Leu	cca Pro	gtt Val	gac Asp	gaa Glu	act Thr	agt Ser	ttg Leu	gac Asp	aag Lys	ggc Gly	act Thr	gat Asp	ttt Phe	927
				195					200					205		
cct Pro	ttg Leu	aaa Lys	tca Ser	gtt Val	acg Thr	gag Glu	acc Thr	gag Glu	aag Lys	ata Ile	gtg Val	ctt Leu	gat Asp	gca Ala	tcc Ser	975
			210					215					220			
ccc Pro	ata Ile	gtt Val	gaa Glu	act Thr	ggg Gly	gat Asp	gac Asp	agt Ser	gtt Val	ata Ile	ggg Gly	tca Ser	cca Pro	tct Ser	gag Glu	1023
		225					230					235				
aat Asn	tta Leu	gag Glu	aca Thr	caa Gln	aag Lys	ctt Leu	caa Gln	gat Asp	ggg Gly	aag Lys	aca Thr	gat Asp	tgt Cys	tca Ser	cca Pro	1071
	240					245					250					
cct Pro	gca Ala	aat Asn	gca Ala	gaa Glu	tcg Ser	aaa Lys	acg Thr	ctg Leu	cca Pro	gtt Val	ggg Gly	gaa Glu	act Thr	agt Ser	tta Leu	1119
255					260					265					270	
gaa Glu	aaa Lys	gaa Glu	tat Tyr	cca Pro	caa Gln	aag Lys	ttt Phe	caa Gln	gat Asp	gat Asp	aac Asn	aca Thr	gat Asp	tgt Cys	cta Leu	1167
				275					280					285		
cca Pro	cct Pro	gca Ala	aat Asn	gca Ala	gaa Glu	tca Ser	aaa Lys	agg Arg	ctg Leu	cca Pro	gtt Val	ggc Gly	gaa Glu	act Thr	agt Ser	1215
			290					295					300			
tta Leu	gaa Glu	aag Lys	gac Asp	act Thr	gat Asp	ttt Phe	cct Pro	ttg Leu	aaa Lys	tca Ser	act Thr	acg Thr	gag Glu	act Thr	gga Gly	1263
		305					310					315				
aag Lys	atg Met	gtt Val	ctt Leu	tat Tyr	gca Ala	tcc Ser	ccc Pro	ata Ile	gtt Val	gaa Glu	act Thr	agg Arg	gat Asp	gac Asp	agc Ser	1311
	320					325					330					
gtt Val	ata Ile	tgt Cys	tca Ser	cca Pro	tct Ser	aca Thr	aat Asn	tta Leu	gaa Glu	acc Thr	caa Gln	aag Lys	ctt Leu	ctt Leu	gtc Val	1359
335					340					345					350	
agt Ser	aaa Lys	act Thr	ggc Gly	tta Leu	gaa Glu	acc Thr	gac Asp	ata Ile	gtt Val	ttg Leu	cct Pro	ttg Leu	aaa Lys	aga Arg	aaa Lys	1407
				355					360					365		
aga Arg	gac Asp	act Thr	gca Ala	gaa Glu	att Ile	gag Glu	ctg Leu	gat Asp	gca Ala	tgt Cys	gct Ala	aca Thr	gtt Val	gca Ala	aat Asn	1455
			370					375					380			
gga Gly	gat Asp	gat Asp	cac His	gtt Val	atg Met	agt Ser	tct Ser	gat Asp	ggg Gly	gtc Val	att Ile	cca Pro	tct Ser	cca Pro	tct Ser	1503
		385					390					395				
ggg Gly	tgc Cys	aaa Lys	aat Asn	gat Asp	aat Asn	cga Arg	cct Pro	gaa Glu	atg Met	tgc Cys	aac Asn	acg Thr	tgt Cys	aaa Lys	aaa Lys	1551
	400					405					410					

cg Arg 415	caa Gln	aag Lys	gtc Val	aac Asn	ggt Gly 420	gat Asp	tgt Cys	caa Gln	aat Asn	agg Arg 425	agt Ser	gtt Val	tgc Cys	tcc Ser	tgc Cys 430	1599
att Ile	gtc Val	cag Gln	cca Pro	gtt Val 435	gaa Glu	gaa Glu	tct Ser	gat Asp	aac Asn 440	gtg Val	aca Thr	cag Gln	gat Asp	atg Met 445	aaa Lys	1647
gaa Glu	act Thr	gga Gly	cca Pro 450	gtt Val	acg Thr	agc Ser	aga Arg	gaa Glu 455	tat Tyr	gag Glu	gag Glu	aac Asn	ggg Gly 460	caa Gln	ata Ile	1695
caa Gln	cat His	ggt Gly 465	aaa Lys	tca Ser	agt Ser	gat Asp	ccc Pro 470	aaa Lys	ttc Phe	tat Tyr	tct Ser	tcg Ser 475	gtg Val	tac Tyr	cca Pro	1743
gag Glu	tat Tyr 480	tg Trp	gtt Val	cct Pro	gtg Val	cag Gln 485	cta Leu	tca Ser	gat Asp	gta Val	cag Gln 490	ctg Leu	gag Glu	caa Gln	tac Tyr	1791
tgt Cys 495	cag Gln	act Thr	ctc Leu	ttc Phe	tcc Ser 500	aaa Lys	tcc Ser	tta Leu	tct Ser	ctt Leu 505	tct Ser	tca Ser	ctt Leu	tcg Ser	aag Lys 510	1839
att Ile	gat Asp	ctt Leu	gga Gly	gct Ala 515	cta Leu	gaa Glu	gaa Glu	act Thr	ctc Leu 520	aat Asn	tct Ser	gta Val	aga Arg	aaa Lys 525	acc Thr	1887
tgt Cys	gac Asp	cat His	cca Pro 530	tac Tyr	gtt Val	atg Met	gat Asp	gca Ala 535	tct Ser	ttg Leu	aaa Lys	caa Gln	ctg Leu 540	ctc Leu	acc Thr	1935
aag Lys	aat Asn	ctg Leu 545	gag Glu	ttg Leu	cat His	gaa Glu	atc Ile 550	ctg Leu	gat Asp	gta Val	gaa Glu	att Ile 555	aaa Lys	gcg Ala	agc Ser	1983
ggg Gly 560	aaa Lys	ctt Leu	cac His	ctc Leu	ctt Leu	gat Asp 565	aaa Lys	atg Met	ctt Leu	act Thr	cat His 570	ata Ile	aaa Lys	aag Lys	aat Asn	2031
ggt Gly 575	tta Leu	aaa Lys	gca Ala	gtt Val	gtc Val 580	ttc Phe	tac Tyr	cag Gln	gca Ala	aca Thr 585	caa Gln	acc Thr	cct Pro	gaa Glu	ggg Gly 590	2079
ctt Leu	ctg Leu	ctt Leu	ggt Gly	aat Asn 595	att Ile	ctc Leu	gaa Glu	gat Asp	ttt Phe 600	gtg Val	ggt Gly	caa Gln	aga Arg	ttt Phe 605	ggt Gly	2127
cca Pro	aaa Lys	tct Ser	tat Tyr 610	gag Glu	cat His	ggg Gly	ata Ile	tat Tyr 615	tcc Ser	tca Ser	aag Lys	aag Lys	aac Asn 620	tcc Ser	gct Ala	2175
ata Ile	aac Asn	aat Asn 625	ttc Phe	aac Asn	aag Lys	gag Glu	agt Ser 630	caa Gln	tgc Cys	tgt Cys	gtt Val	ctg Leu 635	ctg Leu	ttg Leu	gaa Glu	2223
aca Thr 640	cgt Arg	gcc Ala	tgc Cys	agt Ser	caa Gln	acc Thr 645	att Ile	aaa Lys	ctc Leu	ttg Leu	cga Arg 650	gct Ala	gat Asp	gcg Ala	ttt Phe	2271
att Ile 655	ctt Leu	ttt Phe	gga Gly	agc Ser	agc Ser 660	ttg Leu	aat Asn	cca Pro	tcg Ser	cat His 665	gat Asp	gtt Val	aag Lys	cac His	gta Val 670	2319

gag Glu	aag Lys	ata Ile	aaa Lys	atc Ile 675	gag Glu	tca Ser	tgt Cys	tct Ser	gaa Glu 680	aga Arg	act Thr	aag Lys	ata Ile	ttc Phe 685	cga Arg	2367
ttg Leu	tac Tyr	tca Ser	gta Val 690	tgt Cys	aca Thr	gtt Val	gaa Glu	gaa Glu 695	aaa Lys	gcc Ala	ctg Leu	att Ile	ctg Leu 700	gct Ala	agg Arg	2415
caa Gln	aat Asn	atg Met 705	cgg Arg	caa Gln	aat Asn	aaa Lys	gct Ala 710	gta Val	gag Glu	aac Asn	cta Leu	aac Asn 715	cgc Arg	tct Ser	ctc Leu	2463
acg Thr	cac His 720	gca Ala	ctg Leu	ctc Leu	atg Met	tgg Trp 725	ggg Gly	gcg Ala	tca Ser	tac Tyr	tta Leu 730	ttt Phe	gat Asp	aaa Lys	ctg Leu	2511
gat Asp 735	cat His	ttt Phe	cac His	agc Ser	agt Ser 740	gaa Glu	act Thr	cca Pro	gat Asp	tca Ser 745	gga Gly	gtt Val	tca Ser	ttt Phe	gaa Glu 750	2559
caa Gln	tct Ser	att Ile	atg Met	gac Asp 755	ggc Gly	gtg Val	att Ile	cat His	gaa Glu 760	ttc Phe	tcg Ser	tcc Ser	ata Ile	ctt Leu 765	tct Ser	2607
tcc Ser	aaa Lys	ggg Gly	gga Gly 770	gaa Glu	gaa Glu	aat Asn	gaa Glu	gtc Val 775	aag Lys	ctg Leu	tgt Cys	cta Leu	ctt Leu 780	ttg Leu	gag Glu	2655
gcc Ala	aag Lys	cat His 785	gct Ala	cag Gln	gga Gly	act Thr	tac Tyr 790	agc Ser	agt Ser	gat Asp	tct Ser	act Thr 795	cta Leu	ttt Phe	ggg Gly	2703
gaa Glu	gac Asp 800	cat His	att Ile	aag Lys	ttg Leu	tca Ser 805	gat Asp	gaa Glu	gag Glu	agt Ser	cca Pro 810	aat Asn	ata Ile	ttt Phe	tgg Trp	2751
tca Ser 815	aag Lys	ctg Leu	ttg Leu	ggg Gly	gga Gly 820	aaa Lys	aat Asn	cct Pro	atg Met	tgg Trp 825	aaa Lys	tac Tyr	cct Pro	tca Ser	gat Asp 830	2799
act Thr	ccc Pro	caa Gln	agg Arg	aat Asn 835	cga Arg	aaa Lys	cga Arg	gtt Val	cag Gln 840	tat Tyr	ttt Phe	gag Glu	ggg Gly	tct Ser 845	gaa Glu	2847
gcg Ala	agt Ser	ccc Pro	aaa Lys 850	act Thr	ggc Gly	gat Asp	ggg Gly	gga Gly 855	aat Asn	gca Ala	aag Lys	aag Lys	cga Arg 860	aag Lys	aag Lys	2895
gct Ala	tct Ser	gat Asp 865	gat Asp	gtc Val	act Thr	gat Asp	ccc Pro 870	cgg Arg	gtc Val	act Thr	gat Asp	ccg Pro 875	cca Pro	gta Val	gat Asp	2943
gat Asp	gat Asp 880	gaa Glu	aga Arg	aag Lys	gcc Ala	tct Ser 885	ggg Gly	aag Lys	gat Asp	cac His	atg Met 890	ggg Gly	gct Ala	ttg Leu	gag Glu	2991
tca Ser 895	cca Pro	aaa Lys	gtc Val	ata Ile	aca Thr 900	ctc Leu	cag Gln	tca Ser	tca Ser	tgt Cys 905	aaa Lys	tct Ser	tct Ser	ggg Gly	aca Thr 910	3039
gat Asp	ggg Gly	aca Thr	ttg Leu	gat Asp 915	gga Gly	aat Asn	gat Asp	gct Ala	ttt Phe 920	ggc Gly	ttg Leu	tat Tyr	tct Ser	atg Met 925	ggc Gly	3087

agc cat atc tct gga atc cca gag gat atg tta gct agt caa gat tgg	3135
Ser His Ile Ser Gly Ile Pro Glu Asp Met Leu Ala Ser Gln Asp Trp	
930 935 940	
ggg aaa ata ccg gat gaa tca cag agg agg ctc cac act gtt tta aag	3183
Gly Lys Ile Pro Asp Glu Ser Gln Arg Arg Leu His Thr Val Leu Lys	
945 950 955	
ccg aag atg gca aaa ctt tgc caa gtt ttg cat ctt tca gat gct tgc	3231
Pro Lys Met Ala Lys Leu Cys Gln Val Leu His Leu Ser Asp Ala Cys	
960 965 970	
aca agc atg gtc gga aat ttt ctc gaa tat gtt att gaa aat cac cga	3279
Thr Ser Met Val Gly Asn Phe Leu Glu Tyr Val Ile Glu Asn His Arg	
975 980 985 990	
atc tac gaa gag cca gcc act act ttt cag gca ttc cag ata gcc ctg	3327
Ile Tyr Glu Glu Pro Ala Thr Thr Phe Gln Ala Phe Gln Ile Ala Leu	
995 1000 1005	
agt tgg att gca gcc ttg ttg gta aag caa att ctt agc cac aaa gaa	3375
Ser Trp Ile Ala Ala Leu Leu Val Lys Gln Ile Leu Ser His Lys Glu	
1010 1015 1020	
tct ctg gtc cgt gca aat tct gaa tta gct ttc aaa tgc tct aga gta	3423
Ser Leu Val Arg Ala Asn Ser Glu Leu Ala Phe Lys Cys Ser Arg Val	
1025 1030 1035	
gag gtg gat tat att tat tcg ata ttg tcc tgc atg aag agt ctg ttc	3471
Glu Val Asp Tyr Ile Tyr Ser Ile Leu Ser Cys Met Lys Ser Leu Phe	
1040 1045 1050	
ctg gag cat aca caa ggt ttg cag ttc gat tgc ttt ggt act aat tct	3519
Leu Glu His Thr Gln Gly Leu Gln Phe Asp Cys Phe Gly Thr Asn Ser	
1055 1060 1065 1070	
aaa cag tca gtg gtt agc aca aaa cta gta aat gaa agt ctc tca ggg	3567
Lys Gln Ser Val Val Ser Thr Lys Leu Val Asn Glu Ser Leu Ser Gly	
1075 1080 1085	
gct aca gtg cgt gac gaa aag att aat acg aag tcg atg cga aat agc	3615
Ala Thr Val Arg Asp Glu Lys Ile Asn Thr Lys Ser Met Arg Asn Ser	
1090 1095 1100	
tca gag gat gaa gag tgc atg act gag aag aga tgt agc cat tat agc	3663
Ser Glu Asp Glu Glu Cys Met Thr Glu Lys Arg Cys Ser His Tyr Ser	
1105 1110 1115	
aca gca aca aga gat atc gaa aag act att agt ggc ata aaa aag aaa	3711
Thr Ala Thr Arg Asp Ile Glu Lys Thr Ile Ser Gly Ile Lys Lys Lys	
1120 1125 1130	
tac aag aag caa gtg caa aag ctt gta caa gag cat gag gaa aag aaa	3759
Tyr Lys Lys Gln Val Gln Lys Leu Val Gln Glu His Glu Glu Lys Lys	
1135 1140 1145 1150	
atg gag ctg tta aat atg tat gca gac aag aag cag aaa ctt gaa act	3807
Met Glu Leu Leu Asn Met Tyr Ala Asp Lys Lys Gln Lys Leu Glu Thr	
1155 1160 1165	
agt aaa agt gtg gaa gca gca gta att cgt att acc tgt tca cgg acc	3855
Ser Lys Ser Val Glu Ala Ala Val Ile Arg Ile Thr Cys Ser Arg Thr	
1170 1175 1180	

agt act caa gtg ggt gat ctc aaa ctg ctg gat cat aat tat gaa aga	3903
Ser Thr Gln Val Gly Asp Leu Lys Leu Leu Asp His Asn Tyr Glu Arg	
1185 1190 1195	
aag ttt gat gaa atc aaa agt gag aaa aat gaa tgc ctc aaa agt ctg	3951
Lys Phe Asp Glu Ile Lys Ser Glu Lys Asn Glu Cys Leu Lys Ser Leu	
1200 1205 1210	
gag caa atg cac gag gtt gca aag aag aag ttg gct gag gat gaa gcc	3999
Glu Gln Met His Glu Val Ala Lys Lys Lys Leu Ala Glu Asp Glu Ala	
1215 1220 1225 1230	
tgt tgg att aat cgg ata aag agc tgg gca gct aaa tta aaa gtt tgt	4047
Cys Trp Ile Asn Arg Ile Lys Ser Trp Ala Ala Lys Leu Lys Val Cys	
1235 1240 1245	
gtt ccc att caa agt ggc aat aac aag cat ttt agt ggt tca tca aac	4095
Val Pro Ile Gln Ser Gly Asn Asn Lys His Phe Ser Gly Ser Ser Asn	
1250 1255 1260	
att tcc caa aat gct cct gat gta caa att tgc aat aat gct aac gtt	4143
Ile Ser Gln Asn Ala Pro Asp Val Gln Ile Cys Asn Asn Ala Asn Val	
1265 1270 1275	
gaa gct act tac gct gat acg aat tgc atg gct tcc aag gtt aat caa	4191
Glu Ala Thr Tyr Ala Asp Thr Asn Cys Met Ala Ser Lys Val Asn Gln	
1280 1285 1290	
gtg cca gaa gca gaa aac aca tta gga acc atg tgc ggt ggc agc act	4239
Val Pro Glu Ala Glu Asn Thr Leu Gly Thr Met Ser Gly Gly Ser Thr	
1295 1300 1305 1310	
caa caa gtt cat gaa atg gtg gat gta aga aat gac gag aca atg gat	4287
Gln Gln Val His Glu Met Val Asp Val Arg Asn Asp Glu Thr Met Asp	
1315 1320 1325	
gtc tca gct ttg tct cgt gaa cag ctt aca aag agc cag tcc aat gag	4335
Val Ser Ala Leu Ser Arg Glu Gln Leu Thr Lys Ser Gln Ser Asn Glu	
1330 1335 1340	
cac gct tct atc act gtg cct gag att ttg att cct gct gac tgt caa	4383
His Ala Ser Ile Thr Val Pro Glu Ile Leu Ile Pro Ala Asp Cys Gln	
1345 1350 1355	
gag gaa ttt gcg gcc ttg aac gtg cat ttg tca gaa gac cag aat tgt	4431
Glu Glu Phe Ala Ala Leu Asn Val His Leu Ser Glu Asp Gln Asn Cys	
1360 1365 1370	
gac aga ata aca tct gcg gca tca gat gaa gat gtt tca tca agg gtg	4479
Asp Arg Ile Thr Ser Ala Ala Ser Asp Glu Asp Val Ser Ser Arg Val	
1375 1380 1385 1390	
cca gag gta tcc cag tca ctc gaa aat ctt tct gcc tcc ccc gag ttt	4527
Pro Glu Val Ser Gln Ser Leu Glu Asn Leu Ser Ala Ser Pro Glu Phe	
1395 1400 1405	
tct cta aat aga gag gag gct ttg gtt aca aca gaa aat aga aga aca	4575
Ser Leu Asn Arg Glu Glu Ala Leu Val Thr Thr Glu Asn Arg Arg Thr	
1410 1415 1420	
agt cat gtg ggt ttt gat act gat aac att ttg gac cag cag aat aga	4623
Ser His Val Gly Phe Asp Thr Asp Asn Ile Leu Asp Gln Gln Asn Arg	
1425 1430 1435	

gaa gat tgt tct ctt gac caa gag att cct gac gag tta gcg atg cct Glu Asp Cys Ser Leu Asp Gln Glu Ile Pro Asp Glu Leu Ala Met Pro 1440 1445 1450	4671
gtg caa cat ctt gcg tct gtg gta gag act agg ggt gct gct gaa tct Val Gln His Leu Ala Ser Val Val Glu Thr Arg Gly Ala Ala Glu Ser 1455 1460 1465 1470	4719
gat cag tat ggt caa gat ata tgt cct atg cct tct tca ctg gct gga Asp Gln Tyr Gly Gln Asp Ile Cys Pro Met Pro Ser Ser Leu Ala Gly 1475 1480 1485	4767
aag caa cct gac cca gca gca aac act gag agc gaa aat ctt gaa gaa Lys Gln Pro Asp Pro Ala Ala Asn Thr Glu Ser Glu Asn Leu Glu Glu 1490 1495 1500	4815
gca att gag cct cag tct gct ggt tca gaa aca gta gag act act gat Ala Ile Glu Pro Gln Ser Ala Gly Ser Glu Thr Val Glu Thr Thr Asp 1505 1510 1515	4863
ttt gct gca tca cat cag ggt gat caa gtt aca tgt cct ttg cta tct Phe Ala Ala Ser His Gln Gly Asp Gln Val Thr Cys Pro Leu Leu Ser 1520 1525 1530	4911
tca ccg act gga aat cag cct gcg cca gaa gca aat att gaa ggc caa Ser Pro Thr Gly Asn Gln Pro Ala Pro Glu Ala Asn Ile Glu Gly Gln 1535 1540 1545 1550	4959
aat atc aac aca tca gct gag ccc cat gta gcg ggt cca gat gca gta Asn Ile Asn Thr Ser Ala Glu Pro His Val Ala Gly Pro Asp Ala Val 1555 1560 1565	5007
gag agt ggt gat tat gca gta ata gat cag gaa aca atg ggt gct cag Glu Ser Gly Asp Tyr Ala Val Ile Asp Gln Glu Thr Met Gly Ala Gln 1570 1575 1580	5055
gat gca tgc tct ctg cca tct gga tcg gtt gga act cag tct gac cta Asp Ala Cys Ser Leu Pro Ser Gly Ser Val Gly Thr Gln Ser Asp Leu 1585 1590 1595	5103
gga gca aac att gag ggt caa aat gtc aca aca gtg gct caa ctt ccc Gly Ala Asn Ile Glu Gly Gln Asn Val Thr Thr Val Ala Gln Leu Pro 1600 1605 1610	5151
aca gat gga tca gat gca gtt gta acc ggt gga tct cct gta tca gat Thr Asp Gly Ser Asp Ala Val Val Thr Gly Gly Ser Pro Val Ser Asp 1615 1620 1625 1630	5199
cag tgt gcc cag gat gca tct cct atg cca tta tct tcg cct gga aat Gln Cys Ala Gln Asp Ala Ser Pro Met Pro Leu Ser Ser Pro Gly Asn 1635 1640 1645	5247
cac cct gat aca gca gtt aat atc gag ggt tta gat aac aca tca gta His Pro Asp Thr Ala Val Asn Ile Glu Gly Leu Asp Asn Thr Ser Val 1650 1655 1660	5295
gct gag cct cat ata agt gga tca gat gca tgt gaa atg gaa att tca Ala Glu Pro His Ile Ser Gly Ser Asp Ala Cys Glu Met Glu Ile Ser 1665 1670 1675	5343
gaa cct ggt ccc caa gta gag cgg tca acc ttt gca aat ctt ttc cat Glu Pro Gly Pro Gln Val Glu Arg Ser Thr Phe Ala Asn Leu Phe His 1680 1685 1690	5391

gaa ggt ggc gtg gag cat tca gca ggt gta aca gct ctt gtt cca tca	5439
Glu Gly Gly Val Glu His Ser Ala Gly Val Thr Ala Leu Val Pro Ser	
1695 1700 1705 1710	
ctt ctt aac aat ggt acg gaa cag att gcc gtt caa cct gtt cct caa	5487
Leu Leu Asn Asn Gly Thr Glu Gln Ile Ala Val Gln Pro Val Pro Gln	
1715 1720 1725	
ata cct ttc cct gtg ttc aac gac ccg ttt ctg cat gaa ctg gag aag	5535
Ile Pro Phe Pro Val Phe Asn Asp Pro Phe Leu His Glu Leu Glu Lys	
1730 1735 1740	
ttg cgg aga gaa tca gag aac tca aag aag act ttt gaa gaa aaa aaa	5583
Leu Arg Arg Glu Ser Glu Asn Ser Lys Lys Thr Phe Glu Glu Lys Lys	
1745 1750 1755	
tca atc ttg aaa gct gaa ctc gag agg aag atg gct gaa gta caa gca	5631
Ser Ile Leu Lys Ala Glu Leu Glu Arg Lys Met Ala Glu Val Gln Ala	
1760 1765 1770	
gag ttt cga aga aaa ttt cat gag gta gaa gcc gag cat aac acc aga	5679
Glu Phe Arg Arg Lys Phe His Glu Val Glu Ala Glu His Asn Thr Arg	
1775 1780 1785 1790	
acg aca aag ata gag aag gat aag aat ctt gtt ata atg aac aaa ctg	5727
Thr Thr Lys Ile Glu Lys Asp Lys Asn Leu Val Ile Met Asn Lys Leu	
1795 1800 1805	
ttg gcg aat gcg ttc ttg tcc aaa tgt act gac aag aag gta tct ccc	5775
Leu Ala Asn Ala Phe Leu Ser Lys Cys Thr Asp Lys Lys Val Ser Pro	
1810 1815 1820	
tca gga gct cca agg ggt aaa att cag cag cta gca cag aga gca gca	5823
Ser Gly Ala Pro Arg Gly Lys Ile Gln Gln Leu Ala Gln Arg Ala Ala	
1825 1830 1835	
caa gtg agt gca ctg aga aat tac att gct cct cag cag ctt cag gca	5871
Gln Val Ser Ala Leu Arg Asn Tyr Ile Ala Pro Gln Gln Leu Gln Ala	
1840 1845 1850	
tct tct ttt cct gct cct gct ctg gtt tcg gct cct ctg caa ctt cag	5919
Ser Ser Phe Pro Ala Pro Ala Leu Val Ser Ala Pro Leu Gln Leu Gln	
1855 1860 1865 1870	
caa tca tca ttt cct gct cct ggt ccg gct cct ctg cag cct cag gca	5967
Gln Ser Ser Phe Pro Ala Pro Gly Pro Ala Pro Leu Gln Pro Gln Ala	
1875 1880 1885	
tct tcg ttt cct tct tca gtc tct cgt cca tca gcc ctt ctt ctg aat	6015
Ser Ser Phe Pro Ser Ser Val Ser Arg Pro Ser Ala Leu Leu Leu Asn	
1890 1895 1900	
ttt gcg gtc tgt cca atg cct cag ccc aga cag cct ctc ata tcc aac	6063
Phe Ala Val Cys Pro Met Pro Gln Pro Arg Gln Pro Leu Ile Ser Asn	
1905 1910 1915	
ata gct cca act cca tca gtt act cct gca aca aat cca ggt ctg cgt	6111
Ile Ala Pro Thr Pro Ser Val Thr Pro Ala Thr Asn Pro Gly Leu Arg	
1920 1925 1930	
tct cct gca cca cac cta aac tca tat aga cca tcc tct tca act ccc	6159
Ser Pro Ala Pro His Leu Asn Ser Tyr Arg Pro Ser Ser Ser Thr Pro	
1935 1940 1945 1950	

gtc gcc aca gct act cca acc tcg tca gtg cct cct caa gct ttg aca 6207
 Val Ala Thr Ala Thr Pro Thr Ser Ser Val Pro Pro Gln Ala Leu Thr
 1955 1960 1965

tat tca gct gtg tca att cag cag cag caa gaa caa caa ccg caa cag 6255
 Tyr Ser Ala Val Ser Ile Gln Gln Gln Gln Glu Gln Gln Pro Gln Gln
 1970 1975 1980

agc ttg agc agt gga ttg cag agc aac aat gaa gtg gtt tgt ctt tct 6303
 Ser Leu Ser Ser Gly Leu Gln Ser Asn Asn Glu Val Val Cys Leu Ser
 1985 1990 1995

gac gac gag tgacctaga ggagagatgg ttagggctctt agttattgat 6352
 Asp Asp Glu
 2000

ttttagagag ttaataatag tatatatata tatgtataag taggttacct aatctctgtc 6412

gttaatctaa tttagttagt caggaaccga ctcgttggct aaggctcttc cttttgaaac 6472

gcaacgttct actttcatgt atataaatac agtctgatca cacaacacaa attgatgatt 6532

gaaaatacta ctgatttaac ttaaaaaaaaa aaaaaaaaaa 6571

<210> 3
 <211> 2001
 <212> PRT
 <213> Arabidopsis thaliana

<400> 3
 Met Lys Lys Asp Glu Lys Ile Gly Leu Thr Gly Arg Thr Ile Tyr Thr
 1 5 10 15
 Arg Ser Leu Ala Ala Ser Ile Pro Ala Ser Val Glu Gln Glu Thr Pro
 20 25 30
 Gly Leu Arg Arg Ser Ser Arg Gly Thr Pro Ser Thr Lys Val Ile Thr
 35 40 45
 Pro Ala Ser Ala Thr Arg Lys Ser Glu Arg Leu Ala Pro Ser Pro Ala
 50 55 60
 Ser Val Ser Lys Lys Ser Gly Gly Ile Val Lys Asn Ser Thr Pro Ser
 65 70 75 80
 Ser Leu Arg Arg Ser Asn Arg Gly Lys Thr Glu Val Ser Leu Gln Ser
 85 90 95
 Ser Lys Gly Ser Asp Asn Ser Ile Arg Lys Gly Asp Thr Ser Pro Asp
 100 105 110
 Ile Glu Gln Arg Lys Asp Ser Val Glu Glu Ser Thr Asp Lys Ile Lys
 115 120 125
 Pro Ile Met Ser Ala Arg Ser Tyr Arg Ala Leu Phe Arg Gly Lys Leu
 130 135 140
 Lys Glu Ser Glu Ala Leu Val Asp Ala Ser Pro Asn Glu Glu Glu Leu
 145 150 155 160
 Val Val Val Gly Cys Ser Arg Arg Ile Pro Ala Gly Asn Asp Asp Val
 165 170 175

Gln Gly Lys Thr Asp Cys Pro Pro Pro Ala Asp Ala Gly Ser Lys Arg
 180 185 190
 Leu Pro Val Asp Glu Thr Ser Leu Asp Lys Gly Thr Asp Phe Pro Leu
 195 200 205
 Lys Ser Val Thr Glu Thr Glu Lys Ile Val Leu Asp Ala Ser Pro Ile
 210 215 220
 Val Glu Thr Gly Asp Asp Ser Val Ile Gly Ser Pro Ser Glu Asn Leu
 225 230 235 240
 Glu Thr Gln Lys Leu Gln Asp Gly Lys Thr Asp Cys Ser Pro Pro Ala
 245 250 255
 Asn Ala Glu Ser Lys Thr Leu Pro Val Gly Glu Thr Ser Leu Glu Lys
 260 265 270
 Glu Tyr Pro Gln Lys Phe Gln Asp Asp Asn Thr Asp Cys Leu Pro Pro
 275 280 285
 Ala Asn Ala Glu Ser Lys Arg Leu Pro Val Gly Glu Thr Ser Leu Glu
 290 295 300
 Lys Asp Thr Asp Phe Pro Leu Lys Ser Thr Thr Glu Thr Gly Lys Met
 305 310 315 320
 Val Leu Tyr Ala Ser Pro Ile Val Glu Thr Arg Asp Asp Ser Val Ile
 325 330 335
 Cys Ser Pro Ser Thr Asn Leu Glu Thr Gln Lys Leu Leu Val Ser Lys
 340 345 350
 Thr Gly Leu Glu Thr Asp Ile Val Leu Pro Leu Lys Arg Lys Arg Asp
 355 360 365
 Thr Ala Glu Ile Glu Leu Asp Ala Cys Ala Thr Val Ala Asn Gly Asp
 370 375 380
 Asp His Val Met Ser Ser Asp Gly Val Ile Pro Ser Pro Ser Gly Cys
 385 390 395 400
 Lys Asn Asp Asn Arg Pro Glu Met Cys Asn Thr Cys Lys Lys Arg Gln
 405 410 415
 Lys Val Asn Gly Asp Cys Gln Asn Arg Ser Val Cys Ser Cys Ile Val
 420 425 430
 Gln Pro Val Glu Glu Ser Asp Asn Val Thr Gln Asp Met Lys Glu Thr
 435 440 445
 Gly Pro Val Thr Ser Arg Glu Tyr Glu Glu Asn Gly Gln Ile Gln His
 450 455 460
 Gly Lys Ser Ser Asp Pro Lys Phe Tyr Ser Ser Val Tyr Pro Glu Tyr
 465 470 475 480
 Trp Val Pro Val Gln Leu Ser Asp Val Gln Leu Glu Gln Tyr Cys Gln
 485 490 495
 Thr Leu Phe Ser Lys Ser Leu Ser Leu Ser Ser Leu Ser Lys Ile Asp
 500 505 510

Leu Gly Ala Leu Glu Glu Thr Leu Asn Ser Val Arg Lys Thr Cys Asp
 515 520 525
 His Pro Tyr Val Met Asp Ala Ser Leu Lys Gln Leu Leu Thr Lys Asn
 530 535 540
 Leu Glu Leu His Glu Ile Leu Asp Val Glu Ile Lys Ala Ser Gly Lys
 545 550 555 560
 Leu His Leu Leu Asp Lys Met Leu Thr His Ile Lys Lys Asn Gly Leu
 565 570 575
 Lys Ala Val Val Phe Tyr Gln Ala Thr Gln Thr Pro Glu Gly Leu Leu
 580 585 590
 Leu Gly Asn Ile Leu Glu Asp Phe Val Gly Gln Arg Phe Gly Pro Lys
 595 600 605
 Ser Tyr Glu His Gly Ile Tyr Ser Ser Lys Lys Asn Ser Ala Ile Asn
 610 615 620
 Asn Phe Asn Lys Glu Ser Gln Cys Cys Val Leu Leu Leu Glu Thr Arg
 625 630 635 640
 Ala Cys Ser Gln Thr Ile Lys Leu Leu Arg Ala Asp Ala Phe Ile Leu
 645 650 655
 Phe Gly Ser Ser Leu Asn Pro Ser His Asp Val Lys His Val Glu Lys
 660 665 670
 Ile Lys Ile Glu Ser Cys Ser Glu Arg Thr Lys Ile Phe Arg Leu Tyr
 675 680 685
 Ser Val Cys Thr Val Glu Glu Lys Ala Leu Ile Leu Ala Arg Gln Asn
 690 695 700
 Met Arg Gln Asn Lys Ala Val Glu Asn Leu Asn Arg Ser Leu Thr His
 705 710 715 720
 Ala Leu Leu Met Trp Gly Ala Ser Tyr Leu Phe Asp Lys Leu Asp His
 725 730 735
 Phe His Ser Ser Glu Thr Pro Asp Ser Gly Val Ser Phe Glu Gln Ser
 740 745 750
 Ile Met Asp Gly Val Ile His Glu Phe Ser Ser Ile Leu Ser Ser Lys
 755 760 765
 Gly Gly Glu Glu Asn Glu Val Lys Leu Cys Leu Leu Leu Glu Ala Lys
 770 775 780
 His Ala Gln Gly Thr Tyr Ser Ser Asp Ser Thr Leu Phe Gly Glu Asp
 785 790 795 800
 His Ile Lys Leu Ser Asp Glu Glu Ser Pro Asn Ile Phe Trp Ser Lys
 805 810 815
 Leu Leu Gly Gly Lys Asn Pro Met Trp Lys Tyr Pro Ser Asp Thr Pro
 820 825 830
 Gln Arg Asn Arg Lys Arg Val Gln Tyr Phe Glu Gly Ser Glu Ala Ser
 835 840 845
 Pro Lys Thr Gly Asp Gly Gly Asn Ala Lys Lys Arg Lys Lys Ala Ser
 15

850					855					860					
Asp 865	Asp	Val	Thr	Asp	Pro 870	Arg	Val	Thr	Asp	Pro 875	Pro	Val	Asp	Asp	Asp 880
Glu	Arg	Lys	Ala	Ser 885	Gly	Lys	Asp	His	Met 890	Gly	Ala	Leu	Glu	Ser	Pro 895
Lys	Val	Ile	Thr 900	Leu	Gln	Ser	Ser	Cys 905	Lys	Ser	Ser	Gly	Thr 910	Asp	Gly
Thr	Leu	Asp 915	Gly	Asn	Asp	Ala	Phe 920	Gly	Leu	Tyr	Ser	Met 925	Gly	Ser	His
Ile	Ser 930	Gly	Ile	Pro	Glu	Asp 935	Met	Leu	Ala	Ser	Gln 940	Asp	Trp	Gly	Lys
Ile 945	Pro	Asp	Glu	Ser	Gln 950	Arg	Arg	Leu	His	Thr 955	Val	Leu	Lys	Pro	Lys 960
Met	Ala	Lys	Leu	Cys 965	Gln	Val	Leu	His	Leu 970	Ser	Asp	Ala	Cys	Thr 975	Ser
Met	Val	Gly	Asn 980	Phe	Leu	Glu	Tyr	Val 985	Ile	Glu	Asn	His	Arg 990	Ile	Tyr
Glu	Glu	Pro 995	Ala	Thr	Thr	Phe	Gln 1000	Ala	Phe	Gln	Ile	Ala 1005	Leu	Ser	Trp
Ile 1010	Ala	Ala	Leu	Leu	Val	Lys 1015	Gln	Ile	Leu	Ser	His 1020	Lys	Glu	Ser	
Leu 1025	Val	Arg	Ala	Asn	Ser	Glu 1030	Leu	Ala	Phe	Lys	Cys 1035	Ser	Arg	Val	
Glu 1040	Val	Asp	Tyr	Ile	Tyr	Ser 1045	Ile	Leu	Ser	Cys	Met 1050	Lys	Ser	Leu	
Phe 1055	Leu	Glu	His	Thr	Gln	Gly 1060	Leu	Gln	Phe	Asp	Cys 1065	Phe	Gly	Thr	
Asn 1070	Ser	Lys	Gln	Ser	Val	Val 1075	Ser	Thr	Lys	Leu	Val 1080	Asn	Glu	Ser	
Leu 1085	Ser	Gly	Ala	Thr	Val	Arg 1090	Asp	Glu	Lys	Ile	Asn 1095	Thr	Lys	Ser	
Met 1100	Arg	Asn	Ser	Ser	Glu	Asp 1105	Glu	Glu	Cys	Met	Thr 1110	Glu	Lys	Arg	
Cys 1115	Ser	His	Tyr	Ser	Thr	Ala 1120	Thr	Arg	Asp	Ile	Glu 1125	Lys	Thr	Ile	
Ser 1130	Gly	Ile	Lys	Lys	Lys	Tyr 1135	Lys	Lys	Gln	Val	Gln 1140	Lys	Leu	Val	
Gln 1145	Glu	His	Glu	Glu	Lys	Lys 1150	Met	Glu	Leu	Leu	Asn 1155	Met	Tyr	Ala	
Asp 1160	Lys	Lys	Gln	Lys	Leu	Glu 1165	Thr	Ser	Lys	Ser	Val 1170	Glu	Ala	Ala	
Val 1175	Ile	Arg	Ile	Thr	Cys	Ser 1180	Arg	Thr	Ser	Thr	Gln 1185	Val	Gly	Asp	

Leu	Lys	Leu	Leu	Asp	His	Asn	Tyr	Glu	Arg	Lys	Phe	Asp	Glu	Ile
	1190					1195					1200			
Lys	Ser	Glu	Lys	Asn	Glu	Cys	Leu	Lys	Ser	Leu	Glu	Gln	Met	His
	1205					1210					1215			
Glu	Val	Ala	Lys	Lys	Lys	Leu	Ala	Glu	Asp	Glu	Ala	Cys	Trp	Ile
	1220					1225					1230			
Asn	Arg	Ile	Lys	Ser	Trp	Ala	Ala	Lys	Leu	Lys	Val	Cys	Val	Pro
	1235					1240					1245			
Ile	Gln	Ser	Gly	Asn	Asn	Lys	His	Phe	Ser	Gly	Ser	Ser	Asn	Ile
	1250					1255					1260			
Ser	Gln	Asn	Ala	Pro	Asp	Val	Gln	Ile	Cys	Asn	Asn	Ala	Asn	Val
	1265					1270					1275			
Glu	Ala	Thr	Tyr	Ala	Asp	Thr	Asn	Cys	Met	Ala	Ser	Lys	Val	Asn
	1280					1285					1290			
Gln	Val	Pro	Glu	Ala	Glu	Asn	Thr	Leu	Gly	Thr	Met	Ser	Gly	Gly
	1295					1300					1305			
Ser	Thr	Gln	Gln	Val	His	Glu	Met	Val	Asp	Val	Arg	Asn	Asp	Glu
	1310					1315					1320			
Thr	Met	Asp	Val	Ser	Ala	Leu	Ser	Arg	Glu	Gln	Leu	Thr	Lys	Ser
	1325					1330					1335			
Gln	Ser	Asn	Glu	His	Ala	Ser	Ile	Thr	Val	Pro	Glu	Ile	Leu	Ile
	1340					1345					1350			
Pro	Ala	Asp	Cys	Gln	Glu	Glu	Phe	Ala	Ala	Leu	Asn	Val	His	Leu
	1355					1360					1365			
Ser	Glu	Asp	Gln	Asn	Cys	Asp	Arg	Ile	Thr	Ser	Ala	Ala	Ser	Asp
	1370					1375					1380			
Glu	Asp	Val	Ser	Ser	Arg	Val	Pro	Glu	Val	Ser	Gln	Ser	Leu	Glu
	1385					1390					1395			
Asn	Leu	Ser	Ala	Ser	Pro	Glu	Phe	Ser	Leu	Asn	Arg	Glu	Glu	Ala
	1400					1405					1410			
Leu	Val	Thr	Thr	Glu	Asn	Arg	Arg	Thr	Ser	His	Val	Gly	Phe	Asp
	1415					1420					1425			
Thr	Asp	Asn	Ile	Leu	Asp	Gln	Gln	Asn	Arg	Glu	Asp	Cys	Ser	Leu
	1430					1435					1440			
Asp	Gln	Glu	Ile	Pro	Asp	Glu	Leu	Ala	Met	Pro	Val	Gln	His	Leu
	1445					1450					1455			
Ala	Ser	Val	Val	Glu	Thr	Arg	Gly	Ala	Ala	Glu	Ser	Asp	Gln	Tyr
	1460					1465					1470			
Gly	Gln	Asp	Ile	Cys	Pro	Met	Pro	Ser	Ser	Leu	Ala	Gly	Lys	Gln
	1475					1480					1485			
Pro	Asp	Pro	Ala	Ala	Asn	Thr	Glu	Ser	Glu	Asn	Leu	Glu	Glu	Ala
	1490					1495					1500			

Ile	Glu	Pro	Gln	Ser	Ala	Gly	Ser	Glu	Thr	Val	Glu	Thr	Thr	Asp
	1505					1510					1515			
Phe	Ala	Ala	Ser	His	Gln	Gly	Asp	Gln	Val	Thr	Cys	Pro	Leu	Leu
	1520					1525					1530			
Ser	Ser	Pro	Thr	Gly	Asn	Gln	Pro	Ala	Pro	Glu	Ala	Asn	Ile	Glu
	1535					1540					1545			
Gly	Gln	Asn	Ile	Asn	Thr	Ser	Ala	Glu	Pro	His	Val	Ala	Gly	Pro
	1550					1555					1560			
Asp	Ala	Val	Glu	Ser	Gly	Asp	Tyr	Ala	Val	Ile	Asp	Gln	Glu	Thr
	1565					1570					1575			
Met	Gly	Ala	Gln	Asp	Ala	Cys	Ser	Leu	Pro	Ser	Gly	Ser	Val	Gly
	1580					1585					1590			
Thr	Gln	Ser	Asp	Leu	Gly	Ala	Asn	Ile	Glu	Gly	Gln	Asn	Val	Thr
	1595					1600					1605			
Thr	Val	Ala	Gln	Leu	Pro	Thr	Asp	Gly	Ser	Asp	Ala	Val	Val	Thr
	1610					1615					1620			
Gly	Gly	Ser	Pro	Val	Ser	Asp	Gln	Cys	Ala	Gln	Asp	Ala	Ser	Pro
	1625					1630					1635			
Met	Pro	Leu	Ser	Ser	Pro	Gly	Asn	His	Pro	Asp	Thr	Ala	Val	Asn
	1640					1645					1650			
Ile	Glu	Gly	Leu	Asp	Asn	Thr	Ser	Val	Ala	Glu	Pro	His	Ile	Ser
	1655					1660					1665			
Gly	Ser	Asp	Ala	Cys	Glu	Met	Glu	Ile	Ser	Glu	Pro	Gly	Pro	Gln
	1670					1675					1680			
Val	Glu	Arg	Ser	Thr	Phe	Ala	Asn	Leu	Phe	His	Glu	Gly	Gly	Val
	1685					1690					1695			
Glu	His	Ser	Ala	Gly	Val	Thr	Ala	Leu	Val	Pro	Ser	Leu	Leu	Asn
	1700					1705					1710			
Asn	Gly	Thr	Glu	Gln	Ile	Ala	Val	Gln	Pro	Val	Pro	Gln	Ile	Pro
	1715					1720					1725			
Phe	Pro	Val	Phe	Asn	Asp	Pro	Phe	Leu	His	Glu	Leu	Glu	Lys	Leu
	1730					1735					1740			
Arg	Arg	Glu	Ser	Glu	Asn	Ser	Lys	Lys	Thr	Phe	Glu	Glu	Lys	Lys
	1745					1750					1755			
Ser	Ile	Leu	Lys	Ala	Glu	Leu	Glu	Arg	Lys	Met	Ala	Glu	Val	Gln
	1760					1765					1770			
Ala	Glu	Phe	Arg	Arg	Lys	Phe	His	Glu	Val	Glu	Ala	Glu	His	Asn
	1775					1780					1785			
Thr	Arg	Thr	Thr	Lys	Ile	Glu	Lys	Asp	Lys	Asn	Leu	Val	Ile	Met
	1790					1795					1800			
Asn	Lys	Leu	Leu	Ala	Asn	Ala	Phe	Leu	Ser	Lys	Cys	Thr	Asp	Lys
	1805					1810					1815			
Lys	Val	Ser	Pro	Ser	Gly	Ala	Pro	Arg	Gly	Lys	Ile	Gln	Gln	Leu

1820	1825	1830
Ala Gln Arg Ala Ala Gln Val Ser Ala Leu Arg Asn Tyr Ile Ala 1835 1840 1845		
Pro Gln Gln Leu Gln Ala Ser Ser Phe Pro Ala Pro Ala Leu Val 1850 1855 1860		
Ser Ala Pro Leu Gln Leu Gln Gln Ser Ser Phe Pro Ala Pro Gly 1865 1870 1875		
Pro Ala Pro Leu Gln Pro Gln Ala Ser Ser Phe Pro Ser Ser Val 1880 1885 1890		
Ser Arg Pro Ser Ala Leu Leu Leu Asn Phe Ala Val Cys Pro Met 1895 1900 1905		
Pro Gln Pro Arg Gln Pro Leu Ile Ser Asn Ile Ala Pro Thr Pro 1910 1915 1920		
Ser Val Thr Pro Ala Thr Asn Pro Gly Leu Arg Ser Pro Ala Pro 1925 1930 1935		
His Leu Asn Ser Tyr Arg Pro Ser Ser Ser Thr Pro Val Ala Thr 1940 1945 1950		
Ala Thr Pro Thr Ser Ser Val Pro Pro Gln Ala Leu Thr Tyr Ser 1955 1960 1965		
Ala Val Ser Ile Gln Gln Gln Gln Glu Gln Gln Pro Gln Gln Ser 1970 1975 1980		
Leu Ser Ser Gly Leu Gln Ser Asn Asn Glu Val Val Cys Leu Ser 1985 1990 1995		
Asp Asp Glu		

<210> 4
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Oligonucleotide

<400> 4
 catctacggc aatgtaccag c

21

<210> 5
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Oligonucleotide

<400> 5
 gatgggaatt ggctgagtgg c

21

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 6
cagttcctaaa cgtaaaacgg c 21

<210> 7
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide
n= a, t, g, or c; w= a or t

<400> 7
ntcgastwts gwggt 15

<210> 8
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide
n= a, t, g, or c; w= a or t

<400> 8
ngtcgaswga nawgaa 16

<210> 9
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide
n= a, t, g, or c; w= a or t

<400> 9
wgtgnagwan canaga 16

<210> 10
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
20

oligonucleotide
n= a, t, g, or c; w= a or t

<400> 10
wggwancwga wangca 16

<210> 11
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide
n= a, t, g, or c; w= a or t

<400> 11
wgcgwwgawca ngncga 16

<210> 12
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide
n= a, t, g, or c; w= a or t

<400> 12
wgcnagtnag wanaag 16

<210> 13
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide
n= a, t, g, or c; w= a or t

<400> 13
awgcangncw ganata 16

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 14
ctgtacatac tgagtacaat cgga 24

<210> 15
<211> 25

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:Synthetic
 oligonucleotide
 <400> 15
 gcttcaattc ctgcctcagt tgaac 25
 <210> 16
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:Synthetic
 oligonucleotide
 <400> 16
 ctctacgtgc ttaacatcat gcga 24
 <210> 17
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:Synthetic
 oligonucleotide
 <400> 17
 ccagcttctg ctactagaaa gtcag 25
 <210> 18
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:Synthetic
 oligonucleotide
 <400> 18
 ctggagttgc atgaaatcct ggatg 25
 <210> 19
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:Synthetic
 oligonucleotide
 <400> 19
 gctctttgta agctgttcac gagac 25
 <210> 20

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 20
 tcgcatgatg ttaagcacgt agag 24

 <210> 21
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 21
 gagtactggt ccgtgaacag gtaat 25

 <210> 22
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 22
 atgcttgac aagcatgggc ggaaa 25

 <210> 23
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 23
 tgcaacatcg tgcatttgct ccaga 25

 <210> 24
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 24
 cacaagcatg agtttttcct tccgg 25

<210> 25
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 25
ctgactttct agtagcagaa gctgg 25

<210> 26
<211> 519
<212> DNA
<213> Brassica oleracea

<220>
<223> seq1-23
n= a, t, g, or c

<400> 26
gaattcctgn nttacggcat ccttaataga ctgttcaaat ggaactcctg aacctggggg 60
tccactccca tggaagtgtt ccagcttatt aaataaatat gatgcccccc acatgagcaa 120
tgcattgtgt agaggacggg ttaggttctc tagaggctta ttttgccatg caagaatcag 180
ggttttttct tcaactgtta aactgagta caaccggaaa atcttagttc tttcagaaca 240
cgactcaacc tttatcttct ctaagagctt aacgtcatgc gatggattca ggctgcttcc 300
aaaaagtata aaagactcag cgcgtaagag tttaatgctt tgactacagg cacgtatttc 360
cagcagcaga ataaaacact cactctcctt gttgaaattg tttatagcgt tcttcttcga 420
gaggcagacc ccatgctcat aggaattttg accaaatctt tgcattcagaa aatcttcgag 480
aatattacca agcagaagcc cctcagggct atgtattgc 519

<210> 27
<211> 419
<212> DNA
<213> Brassica oleracea

<220>
<223> seq1-27

<400> 27
gaattcagga tcaaaagggt tgccgggttg agaaactggt ttagagaaag gctctgattt 60
tcctgtggaa gtaactaagg atatagagaa gacagtgggt gattcatccc ccatgggtga 120
aactgaggat ggcagtgtta taggttcacc atccgagaat ccagaaccac aaaagcttcg 180
tgacagttaa actagcttgg aaaccgatat agacttggct ctgaaaagaa aaagagacac 240
tgcagaaatt gtgatggatg catgtacaaa tgcagatgac cgcattatga gtactgatgg 300
ggttatttct tttccaccg tgtgcacaaa tattaatcaa cccgaaagggt gtggcacatg 360
tcaaaaacgg caaaagtaag aatttccgac tgttgtctgt cgttttgaaa ccatttgcc 419

<210> 28
<211> 467
<212> DNA
<213> Brassica oleracea

<220>
<223> seq1-43

<400> 28
gaattctcgt ccatactttc ttccgatgtt ggagaagaaa atgaaggcaa gctgtgtcta 60
cttttggaag ccaagcatgc tcagggaagt tacagcactg atgctactct atttgggtgaa 120
gaacatgtca agttatcaga tgaaagtcca aatatgtttt ggtcaaagct gttgagtgga 180

aagaacccta	tgtggaaata	ctgttcggat	actcctcaaa	ggagtcgaaa	aagagtacgg	240
catcttcagg	gctatgagga	gactaccaaa	gttggcaatg	gcggaaactt	aaagaagaaa	300
aagaaggctt	cagatgatgt	cacagtagat	aacgctgaga	gaaaagcctc	tggaaaggat	360
cacatgggta	aaacagttca	cttcctgctc	ctttacctct	agtgttcatt	gaatgttcca	420
tttactttgc	ttactatctt	tccttcaggg	catttggagt	caccaa		467

<210> 29
 <211> 490
 <212> DNA
 <213> Brassica oleracea

<220>
 <223> seq1-47

<400> 29						
gaattcagct	tttaaaactg	atctctgctc	acagataatt	taagagtcag	tgaaaattga	60
gataaaacga	acaaaaactg	gaggtaacag	atactctgag	aacaactaac	cttttcttca	120
taagtcttct	ttgtgttctc	tgattctctc	cgcagcttct	ccagttcatg	ctgaaatggg	180
tcactgaaca	cagggaaagg	tacttgagga	acaggtggag	tggcattctg	tcccgtagca	240
ttgttaagct	gtgaagaaac	aggagctggt	acacctgctg	gaggctccac	aacaccttca	300
tcgacaacgt	ctgcgtaaaa	ggtattacca	gattgtcagt	ttctctggca	aacacatacg	360
ttatacttaa	atgcaaaaga	gcagttactg	acttgcaaag	gttggttgtt	ctacttgagc	420
atcaggttct	gctacttcca	tttcacatgc	ttctgatcca	gttgtgagag	gcgcagccat	480
tggtgtgttg						490

<210> 30
 <211> 515
 <212> DNA
 <213> Brassica oleracea

<220>
 <223> 2-33

<400> 30						
tctagagaag	aggtggatta	tgtatattct	tttctgtact	gcatgaagag	tctatttcgtg	60
gggcgcacac	aaggtttcca	agaaaagggt	gaagaatgca	tggctgagaa	aagaggtagc	120
cattatagct	cagtaaccaa	ggatgttgaa	aagactatta	gcgacatcaa	aaagaaatgc	180
agtaagagcc	tgcataagct	tgtacaaacc	ctcgagggaag	aaaagatgga	cctgatgaat	240
aggaatgctg	tcaagaagca	ggaacttcag	aattgtaaaa	aggtggaagc	atcatttatt	300
cgtgtcacct	attcaggtat	aaatactcag	agcttacatg	atgctctcca	acggctggaa	360
tgtacttttg	aaagaaaagt	tgatgatctc	aaaggagagt	tggatgaatg	ccttgaaaagt	420
ttagagcaaa	taaacgaggc	tggaaagaag	aagttggctg	aagatgaagc	ctgttggatt	480
agtcggatag	agaaatgggc	acgagctgaa	ttaag			515

<210> 31
 <211> 574
 <212> DNA
 <213> Brassica oleracea

<220>
 <223> seq2-37

<400> 31						
tctagaccaa	actattnaac	gctaaacata	agaagattag	atcactcgtc	atcagagaga	60
cagaccacat	cattgctcct	ctgcaatcca	ctccccaagt	tctgtggttg	ttcttgctgc	120
tgaataaacg	catttgaata	tggtaaaggg	ttggagatga	gaggttgtct	tggttgaggc	180
attgtgcagt	acggagccga	agcagtatga	ttcctcagtg	cgcttacttg	tggtgctctc	240
tgtgctagct	gctggattct	aactggagaa	agaaaaaaag	aaaaaaaagg	tgttattatg	300
acttcataac	cttatatctt	taaaaaacaa	ttatgcttct	attattcgaa	cacttgccca	360
ttggagttgc	tgctgaggaa	tgagaggaga	ttctgctcgt	acatttagac	aagaacgcac	420
tcgacaacag	cttgttcttt	ataacaagat	tcttcctcgt	ctgtaacttc	gtctttctg	480

ctgcatgtac agcttgtacc tcatgaaact ttctctgata ctcttcttgt aattcagcta 540
tcttcttctc gaatttagct ttcaagactg cttt 574

<210> 32
<211> 466
<212> DNA
<213> Brassica oleracea

<220>
<223> seq2-53

<400> 32
tctagattgt aattttaaat ttacaacaaa ttttgaaagg gtcagcgatg agtttgcaaa 60
tctccgtgtt tcctccagca ttgctcagcc agttcaagaa cctgatcact tggcacaggt 120
tggtttcttc ttgctttact ttggacacct gtttaatat ggctgtcaa atttacttat 180
ccttttactt ctaaactgca aattctgggtc tgcattgcat tgtgatatga aggtatctgg 240
acccgcttca agcagagact atggggagga caggcagaat atgcaacaag ataaatcaca 300
tgaccgaaag ttgtcatcga tgtatccaga gtattgggtt ccagtgcagc tatcagatgt 360
acagatagag caatactgtc ggactctctt ctccaaatct tcatctcttt cttcgctgtc 420
gaggactgat cctgttcgag ctcttgaaca aactctcagt tctgta 466

<210> 33
<211> 417
<212> DNA
<213> Brassica oleracea

<220>
<223> seq2-57

<400> 33
tctagagcaa ttgaaaccta attccgattt tgcgcggggc agagattctt cacggttgaa 60
cttttgctta acgaaagaga ctgcaatcca aatctggaag tgcattatta agaacgtatt 120
cagcaatatt cataaattat gcaacaatca aaggccttac gttgtggcct acaaagcatg 180
gattttgtta gatattagta gctagtctaa ttcaagcaat taatggaagt ttctatccta 240
tgactggaaa gttaaacatt cccacaaaag cagtgatgcc acagatgatg aagaagaaaa 300
atgcatatac tatggaagtg aatgctatca taccacagct atctggaagg cctgcaatgt 360
tgtagctggc tctttgcaga cacggtgggt gtcaataata tattcaagaa ctttttc 417